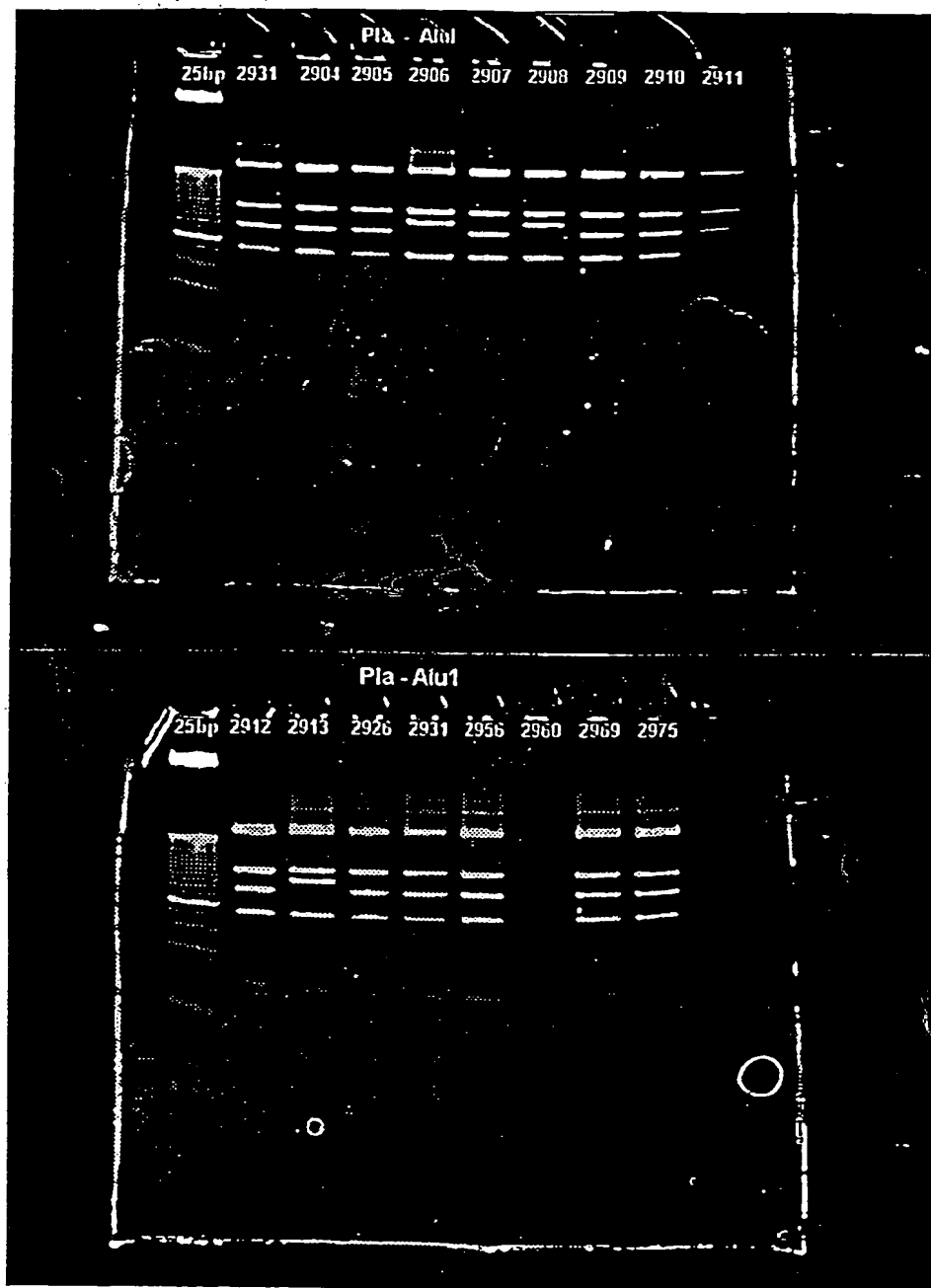
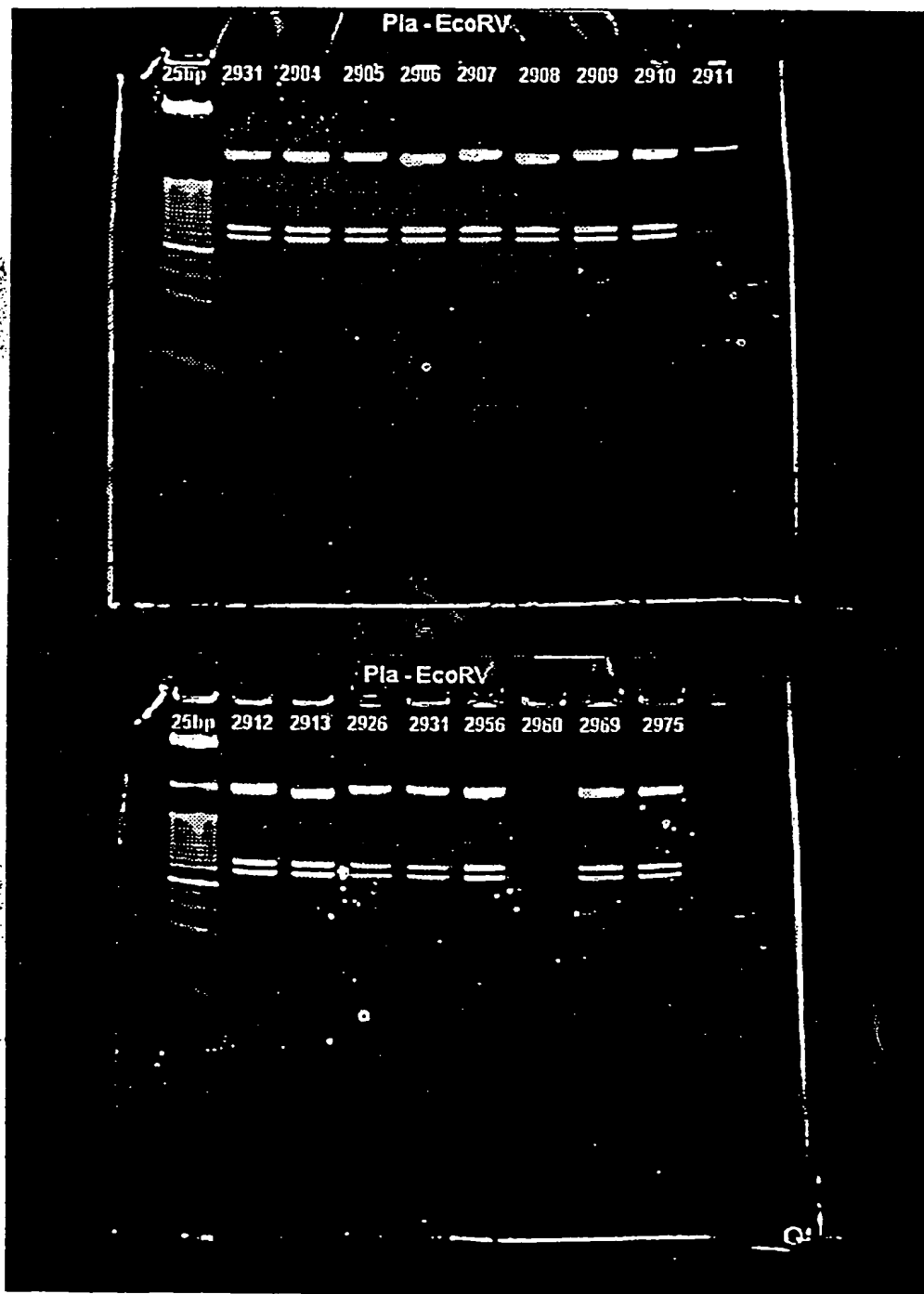


Figure 1 : Photographs of the electrophoresis gels obtained in the RFLP analysis of BASB034



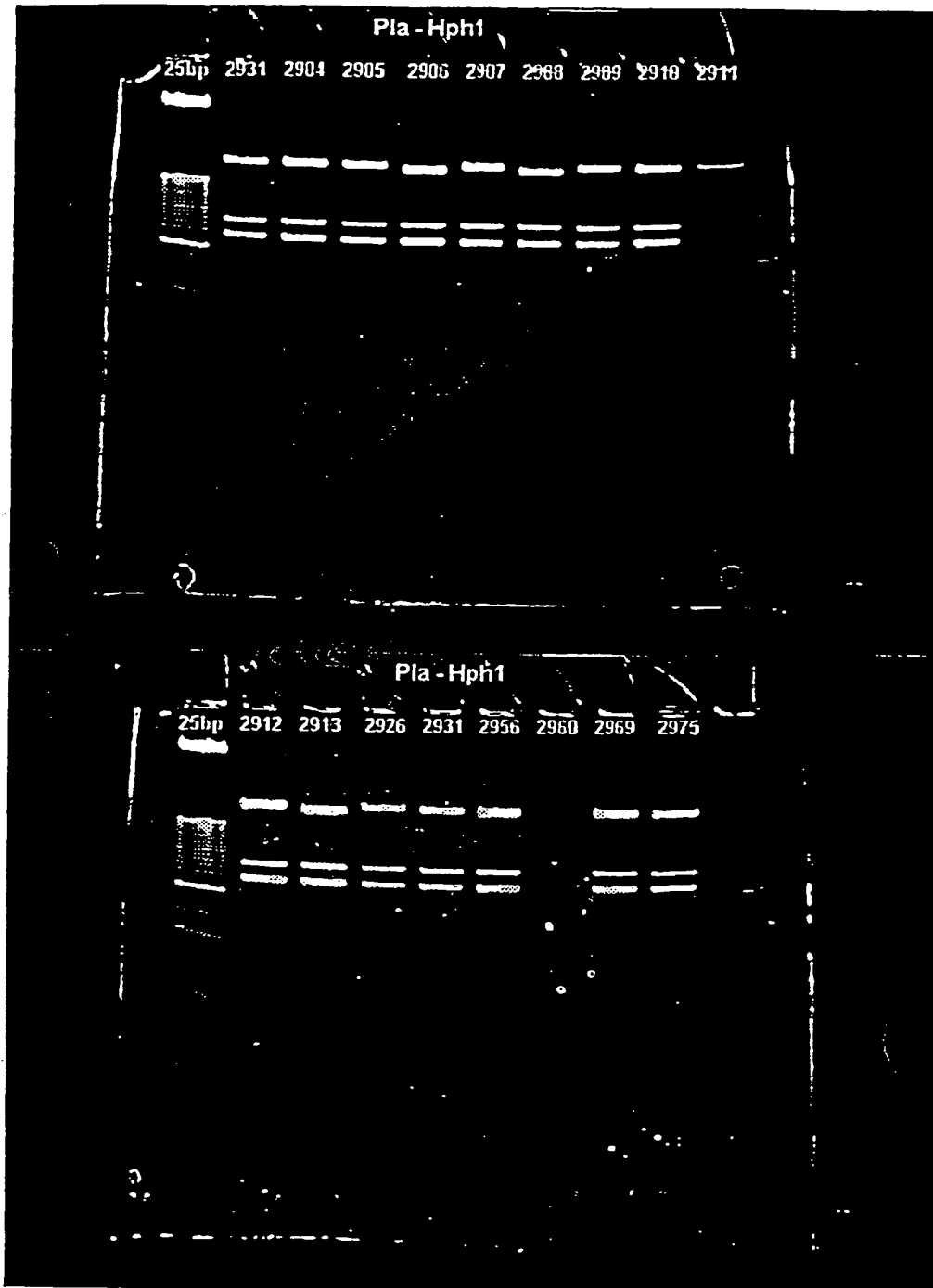
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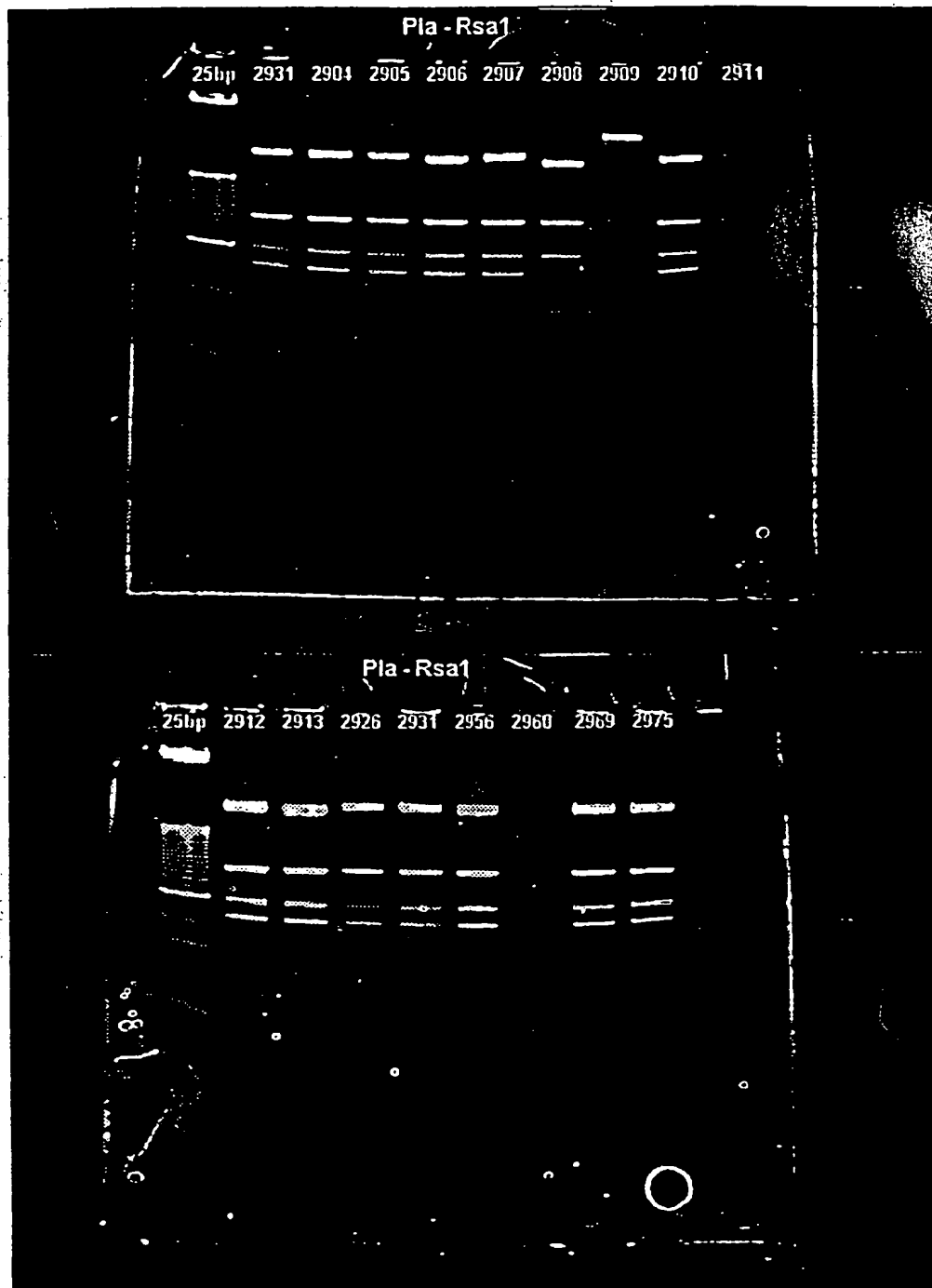


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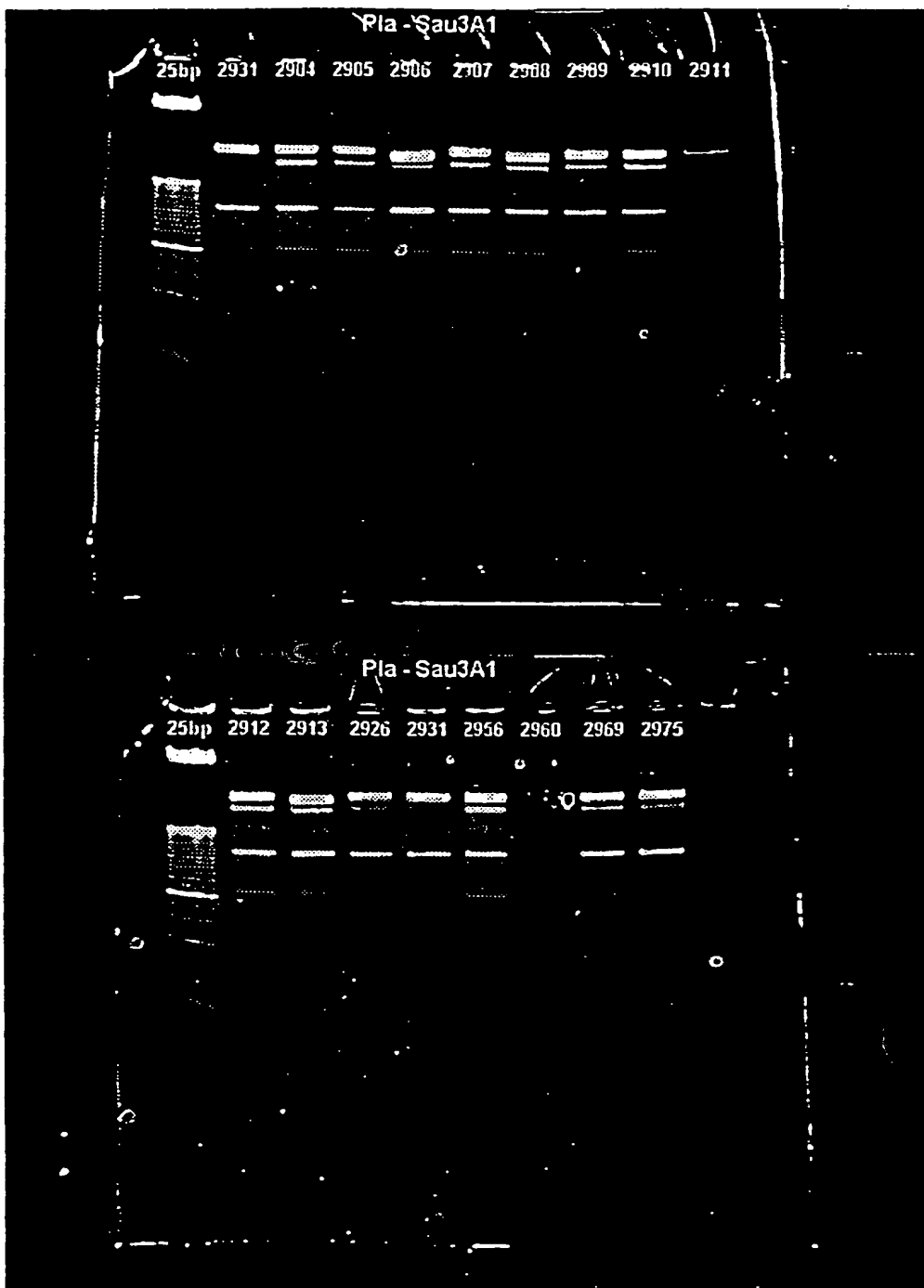


Figure 2 : Alignment of the BASB034 polynucleotide sequences.

Identity to SeqID No:1 is indicated by a dot.

		*	20	*	40	*	
Seqid1 :	ATGAAAGTTTCACTGTCTACATTGACTTTATCTATTTTGTCAATGTTTGC :						50
Seqid3 :	.....C.....						50
Seqid5 :	.....						50
Seqid7 :	.....C.....						50
			60	*	80	*	100
Seqid1 :	TATCCTAGCCATTGAGCAAGCACAAGCTGTACCAATCCTGTGGCATTG :						100
Seqid3 :	.....						100
Seqid5 :	.....A.....						100
Seqid7 :	C.....						100
		*	120	*	140	*	
Seqid1 :	TTGACGAAGTACGCAGTGAAATGATCTTGGGCAAGACAATGAATTACCC :						150
Seqid3 :	.....A.....T.						150
Seqid5 :	.....						150
Seqid7 :	.....						150
			160	*	180	*	200
Seqid1 :	ATTGATGTCCAAAGTGCACACAATCAGCGTCTACTGATACGGCTAATCC :						200
Seqid3 :	....G...A.....						200
Seqid5 :	.....						200
Seqid7 :	.....G.....						200
		*	220	*	240	*	
Seqid1 :	TTTAGACGAACATGAACCAGAGCTTTATACGACAGCTTTAGAAAATAAAA :						250
Seqid3 :	.....						250
Seqid5 :	.....						250
Seqid7 :	.....						250

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260 \* 280 \* 300  
Seqid1 : CCATGCTGATTAAGTCTCAGCACTTAATCAAGATATCATGCGTTTGGCG : 300  
Seqid3 : ..... : 300  
Seqid5 : ..... : 300  
Seqid7 : ..... : 300

\* 320 \* 340 \*  
Seqid1 : TGCTATGACACTTTGGTGCATGGTGAGACGCCAGCGGTAATTAAACCAA : 350  
Seqid3 : ..... : 350  
Seqid5 : ..... : 350  
Seqid7 : ..... : 350

360 \* 380 \* 400  
Seqid1 : GCGTTCATTTCGCCTTGATGAAACAATTTGGCAGACCATCAAAGGCAAAC : 400  
Seqid3 : ..... : 400  
Seqid5 : ..... : 400  
Seqid7 : ..... : 400

\* 420 \* 440 \*  
Seqid1 : CCCAGGTTATCTATCAAGAAACGACAGATCCGATTTTTTAATGGGTAAT : 450  
Seqid3 : .....G..... : 450  
Seqid5 : .....G..... : 450  
Seqid7 : .....G..... : 450

460 \* 480 \* 500  
Seqid1 : GAAAAAGGCATGCTGACCAAAAAAGATGCCAACAGCTTGAATATGCAGC : 500  
Seqid3 : ..... : 500  
Seqid5 : ..... : 500  
Seqid7 : ..... : 500

\* 520 \* 540 \*  
Seqid1 : CAAACAGTTTACACCACTGAGCTTATCATTGATTGACCGAAATAATA : 550

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Seqid3 : ..... : 550  
 Seqid5 : ..... : 550  
 Seqid7 : ..... : 550

560 \* 580 \* 600  
 Seqid1 : CACCACTTTGGTCATCACGACCACACAATCCGATGTATGTATTGCCATA : 600  
 Seqid3 : ....G..... : 600  
 Seqid5 : ..... : 600  
 Seqid7 : ..... : 600

\* 620 \* 640 \*  
 Seqid1 : TTTATGCACGGTAAGCCTAATCGAAGCCCAAATACGCCCAGTCATGAAGC : 650  
 Seqid3 : ..... : 650  
 Seqid5 : ..... : 650  
 Seqid7 : ..... : 650

660 \* 680 \* 700  
 Seqid1 : AAAACAATTTACCCCAAATGAATTCGTGCTCCCGAGCTAAAATTCAGG : 700  
 Seqid3 : ..G.....C..T..AT.....A. : 700  
 Seqid5 : ..G.....C..T..AT.....A. : 700  
 Seqid7 : ..... : 700

\* 720 \* 740 \*  
 Seqid1 : TTTCTGTAAAGGTTAAAGCTGCTGAGGATTTATGGGGACGGATTCAGAT : 750  
 Seqid3 : ..... : 750  
 Seqid5 : ..... : 750  
 Seqid7 : ..... : 750

760 \* 780 \* 800  
 Seqid1 : TTATGGTTTGGATATACACAGCAATCGCACTGGCAGATTTTAAATGGAAA : 800  
 Seqid3 : .....G..... : 800  
 Seqid5 : ..... : 800  
 Seqid7 : ..... : 800

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\*            820                                \*            840                                \*

Seqid1 : AAACCTCTCGTCCTTTTAGAGTACATGACTACCAGCCAGAGATTTTCTTAA : 850

Seqid3 : .....T..... : 850

Seqid5 : .....T..... : 850

Seqid7 : ..... : 850

                             860                                \*            880                                \*            900

Seqid1 : CTCAACCTGTATACTCAGACTTACCATGGGATGGCAAAGTCCGCATGATT : 900

Seqid3 : .....G..... : 900

Seqid5 : ..... : 900

Seqid7 : ..... : 900

                             \*            920                                \*            940                                \*

Seqid1 : GGCATGGGTGCGGTACATCATTCCAATGGTGAAAGTGCCAAACTGTCTCG : 950

Seqid3 : ..... : 950

Seqid5 : ..... : 950

Seqid7 : ..... : 950

                             960                                \*            980                                \*            1000

Seqid1 : CTCATGGAATCGTGCTTATTTGATGGCAGGCATGGAATGGAAAAACCTGA : 1000

Seqid3 : ..... : 1000

Seqid5 : ..... : 1000

Seqid7 : ..... : 1000

                             \*            1020                                \*            1040                                \*

Seqid1 : CTGTCATGCCACGCATTTGGGGCGTATCTTTAAAGAGGGTAGTGGCAGC : 1050

Seqid3 : ..... : 1050

Seqid5 : ..... : 1050

Seqid7 : ..... : 1050

                             1060                                \*            1080                                \*            1100

Seqid1 : CAGCCAGATGATAATCCTGATATCTTGACTATTATGGTTATGGTGATGT : 1100

Seqid3 : .....C..... : 1100

Seqid5 : .....C..... : 1100

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Seqid7 : ..... : 1100

\* 1120 \* 1140 \*

Seqid1 : GCGTTTTTATATCAACTAGAAAAATAAAAGTAATATTTTCAGGTACGGTAC : 1150

Seqid3 : ..... : 1150

Seqid5 : ..... : 1150

Seqid7 : ..... : 1150

1160 \* 1180 \* 1200

Seqid1 : GCTATAATCCACGCTCAGGCAAAGGTGCGTTGCAACTTGACTATGTCTAT : 1200

Seqid3 : ..... : 1200

Seqid5 : ..... : 1200

Seqid7 : ..... : 1200

\* 1220 \* 1240 \*

Seqid1 : CCGCTTGGTAAAGGAATTAGTGGCTATTTTCAAATATTTCAAGGCTATGG : 1250

Seqid3 : ..... : 1250

Seqid5 : ..... : 1250

Seqid7 : ..... : 1250

1260 \* 1280 \* 1300

Seqid1 : GCAGTCTTTGATTGATTATAATCATGAGGCGACAAGCTTTGGCGTCGGAC : 1300

Seqid3 : ..... : 1300

Seqid5 : ..... : 1300

Seqid7 : ..... : 1300

\* 1320

Seqid1 : TTATGCTTAACGACTGGATGGGTCTATAA : 1329

Seqid3 : ..... : 1329

Seqid5 : ..... : 1329

Seqid7 : ..... : 1329

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Figure 3 : Alignment of the BASB034 polypeptide sequences.

Identity to SeqID No:2 is indicated by a dot.

```

      *      20      *      40      *
Seqid2 : MKVSLSTLTLSILSCFAILAIQQAQAVPNPVAFFVDEVRSENDLGQDNELP : 50
Seqid4 : .....P.....K.....L : 50
Seqid6 : .....K..... : 50
Seqid8 : .....P..... : 50

      60      *      80      *      100
Seqid2 : IDVQSATQSASTDTANPLDEHEPELYTTALENKTMLINCSALNQDIMRLA : 100
Seqid4 : .G..... : 100
Seqid6 : ..... : 100
Seqid8 : ..... : 100

      *      120      *      140      *
Seqid2 : CYDTLVHGETPAVIKTKRSIRLDETIWQTIKGKQVIYQETTDPIFLMGN : 150
Seqid4 : .....V..... : 150
Seqid6 : .....V..... : 150
Seqid8 : .....V..... : 150

      160      *      180      *      200
Seqid2 : EKGMLTKKDAKQLEYAAKQFTPLSLSFOLDNRNNTPLWSSRPHPNPMYVLPI : 200
Seqid4 : ..... : 200
Seqid6 : ..... : 200
Seqid8 : ..... : 200

      *      220      *      240      *
Seqid2 : FMHGKPNRSPNTPSHEAKQFTPNEFRAPELKFQVSVKVKAAEDLWGTDSO : 250
Seqid4 : .....R..... : 250
Seqid6 : .....R..... : 250
Seqid8 : ..... : 250
```

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260                   \*                   280                   \*                   300  
Seqid2 : LWFGYTQQSHWQIFNGKNSRPFVRVHDYQPEIFLTQPVYSDLPWDGKVRMI : 300  
Seqid4 : ..... : 300  
Seqid6 : ..... : 300  
Seqid8 : ..... : 300

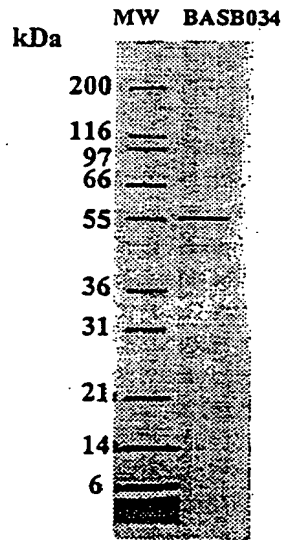
                                         \*                   320                   \*                   340                   \*  
Seqid2 : GMGAVHHSNGESAKLSRSWNRAYLMAGMEWKNLTVMPRIWGRIFKEGSGS : 350  
Seqid4 : ..... : 350  
Seqid6 : ..... : 350  
Seqid8 : ..... : 350

                                         360                   \*                   380                   \*                   400  
Seqid2 : QPDDNPDILDYGYGDVRFYQLENKSNISGTVRYNPRSGKALQLDYVY : 400  
Seqid4 : ..... : 400  
Seqid6 : ..... : 400  
Seqid8 : ..... : 400

                                         \*                   420                   \*                   440  
Seqid2 : PLGKGISGYFQIFQGYGQSLIDYNHEATSFGVGLMLNDWMGL : 442  
Seqid4 : ..... : 442  
Seqid6 : ..... : 442  
Seqid8 : ..... : 442

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Figure 4 : Coomassie stained SDS-PAGE of recombinant purified BASB034

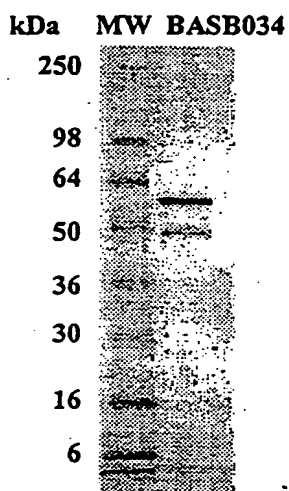


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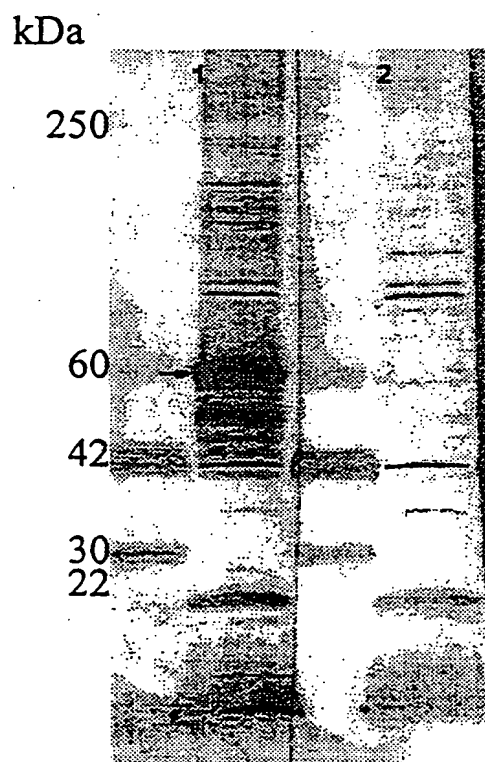
**Figure 5 : Western-blot of purified recombinant BASB034 protein probed with anti-His antibody**



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Figure 6 : Western-blot of BASB034 probed with immune (membrane 1; right lane) and pre-immune (membrane 2; right lane) rabbit sera at 1:500. The arrow indicates the position of BASB034 on the membrane. The left lanes on membrane 1 and 2 are molecular weight markers.



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